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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/484,629A

DATE: 04/17/2001
 TIME: 20:04:31

Input Set : A:\robinson.txt
 Output Set: N:\CRF3\04172001\I484629A.raw

3 <110> APPLICANT: Medical Research Council
 5 <120> TITLE OF INVENTION: Obesity Gene
 7 <130> FILE REFERENCE: 18396/1140
 9 <140> CURRENT APPLICATION NUMBER: 09/484,629A
 10 <141> CURRENT FILING DATE: 2000-01-18
 12 <150> PRIOR APPLICATION NUMBER: GB 9910522.3
 13 <151> PRIOR FILING DATE: 1999-05-06
 15 <160> NUMBER OF SEQ ID NOS: 46
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 924
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Rattus sp.
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (5)..(607)
 28 <400> SEQUENCE: 1

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30	Met	Leu	Arg	Ala	Leu	Asn	Arg	Leu	Ala	Ala	Arg	Pro	Gly	Gly	Gln	
31	1								5						15	
33	ccc	cca	acc	ctg	ctc	ctt	ctg	ccc	gtg	cgc	ggc	cgc	aag	acc	cgc	97
34	Pro	Pro	Thr	Leu	Leu	Leu	Leu	Pro	Val	Arg	Gly	Arg	Lys	Thr	Arg	His
35								20		25				30		
37	gat	ccg	cct	gcc	aag	tcc	aag	gtc	ggg	cgc	gtg	aaa	atg	cct	cct	145
38	Asp	Pro	Pro	Ala	Lys	Ser	Lys	Val	Gly	Arg	Val	Lys	Met	Pro	Pro	Ala
39					35				40			45				
41	gtg	gac	cct	gcg	gaa	ttg	ttc	gtg	ttg	acc	gag	cgc	tac	cga	cag	193
42	Val	Asp	Pro	Ala	Glu	Leu	Phe	Val	Leu	Thr	Glu	Arg	Tyr	Arg	Gln	Tyr
43					50				55			60				
45	cgg	gag	acg	gtg	cgc	gct	ctc	agg	cga	gag	ttc	aca	ttg	gag	gtg	241
46	Arg	Glu	Thr	Val	Arg	Ala	Leu	Arg	Arg	Glu	Phe	Thr	Leu	Glu	Val	Arg
47								70			75					
49	ggg	aaa	ttg	cac	gag	gcc	cga	gcc	ggg	gtt	ctg	gct	gag	cgc	aag	289
50	Gly	Lys	Leu	His	Glu	Ala	Arg	Ala	Gly	Val	Leu	Ala	Glu	Arg	Lys	Ala
51	80					85				90			95			
53	caa	gag	gcc	atc	aga	gag	cac	cag	gag	ctg	atg	gcc	tgg	aac	cgg	337
54	Gln	Glu	Ala	Ile	Arg	Glu	His	Gln	Glu	Leu	Met	Ala	Trp	Asn	Arg	Glu
55						100			105			110				
57	gag	aac	cgg	aga	ctg	cag	gaa	cta	cgg	ata	gct	agg	ttg	cag	ctc	385
58	Glu	Asn	Arg	Arg	Leu	Gln	Glu	Leu	Arg	Ile	Ala	Arg	Leu	Gln	Leu	Glu
59						115			120			125				
61	gca	cag	gcc	cag	gag	ctg	cgg	cag	gct	gag	gtc	cag	gcc	cag	agg	433
62	Ala	Gln	Ala	Gln	Glu	Leu	Arg	Gln	Ala	Glu	Val	Gln	Ala	Gln	Arg	Ala
63						130		135			140					
65	cag	gag	gag	cag	gag	gtc	ttg	caa	ctg	aaa	gaa	caa	gaa	gtt	ctc	481
66	Gln	Glu	Gln	Ala	Trp	Val	Gln	Leu	Lys	Glu	Gln	Glu	Val	Leu	Lys	
67						145		150			155					

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69	ctg	cag	gag	gag	gcc	aaa	aac	ttc	atc	act	cg	gag	aac	ctg	gag	gca	529
70	Leu	Gln	Glu	Glu	Ala	Lys	Asn	Phe	Ile	Thr	Arg	Glu	Asn	Leu	Glu	Ala	
71	160		165						170						175		
73	cgg	ata	gaa	gag	gcc	ttg	gac	tct	ccg	aag	agt	tat	aac	tgg	gcg	gtc	577
74	Arg	Ile	Glu	Glu	Ala	Leu	Asp	Ser	Pro	Lys	Ser	Tyr	Asn	Trp	Ala	Val	
75			180						185					190			
77	acc	aaa	gaa	ggg	cag	gtg	gtc	agg	aac	tga	'gaacagaggc	ctctcaggcc					627
78	Thr	Lys	Glu	Gly	Gln	Val	Val	Arg	Asn								
79			195				200										
81	caaataagga	cagtgc	ttgc	ctaggactg	gatattgggg	tagaaattgg	tgc	atcccag									687
83	gagggtggca	cagc	cattgtc	cagacagcc	cccatcatt	ctagatttg	cac	caggat									747
85	agtacctgtt	ctg	acaccac	atacaaactc	cgacac	cat	taaactctgg	gaagt	tccta								807
87	tcacacagaa	gatc	agactg	actgtcccc	tctagaagcc	aagag	ctgtc	tctg	gagttt								867
89	cttggatag	tgt	gagccca	atgtttcctg	cttttataaa	taaa	actattt	gaa	agca								924
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94	<212>	TYPE:	PRT														
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100	1				5				10					15			
103	Pro	Thr	Leu	Leu	Leu	Leu	Pro	Val	Arg	Gly	Arg	Lys	Thr	Arg	His	Asp	
104					20			25				30					
107	Pro	Pro	Ala	Lys	Ser	Lys	Val	Gly	Arg	Val	Lys	Met	Pro	Pro	Ala	Val	
108			35				40				45						
111	Asp	Pro	Ala	Glu	Leu	Phe	Val	Leu	Thr	Glu	Arg	Tyr	Arg	Gln	Tyr	Arg	
112			50			55			60								
115	Glu	Thr	Val	Arg	Ala	Leu	Arg	Arg	Glu	Phe	Thr	Leu	Glu	Val	Arg	Gly	
116	65				70			75			80						
119	Lys	Leu	His	Glu	Ala	Arg	Ala	Gly	Val	Leu	Ala	Glu	Arg	Lys	Ala	Gln	
120					85			90			95						
123	Glu	Ala	Ile	Arg	Glu	His	Gln	Glu	Leu	Met	Ala	Trp	Asn	Arg	Glu	Glu	
124			100			105			110								
127	Asn	Arg	Arg	Leu	Gln	Glu	Leu	Arg	Ile	Ala	Arg	Leu	Gln	Leu	Glu	Ala	
128			115			120			125								
131	Gln	Ala	Gln	Glu	Leu	Arg	Gln	Ala	Glu	Val	Gln	Ala	Gln	Arg	Ala	Gln	
132			130			135			140								
135	Glu	Glu	Gln	Ala	Trp	Val	Gln	Leu	Lys	Glu	Gln	Glu	Val	Leu	Lys	Leu	
136	145					150			155			160					
139	Gln	Glu	Glu	Ala	Lys	Asn	Phe	Ile	Thr	Arg	Glu	Asn	Leu	Glu	Ala	Arg	
140					165			170			175						
143	Ile	Glu	Glu	Ala	Leu	Asp	Ser	Pro	Lys	Ser	Tyr	Asn	Trp	Ala	Val	Thr	
144					180			185			190						
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154	<213>	ORGANISM:	Rattus sp.														

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156 <220> FEATURE:
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (1)..(996)
160 <400> SEQUENCE: 3
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162 Met Leu Arg Ala Leu Ser Arg Leu Gly Ala Gly Thr Pro Cys Arg Pro
163 1           5           10          15
164           20          25          30
165 cggtt ggc cct ctg gtg ctg cca gcg cgc ggc aag acc ccg cac gac        96
166 Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp
167           20          25          30
168           35          40          45
169 ccgtt gcc aaa tcc aag atc gag cga gtg aac atg ccg ccc gcg gtg        144
170 Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val
171           35          40          45
172           50          55          60
173 gac cct gcg gag ttc ttc gtg ctg atg gag cgt tac cag cac tac cgc        192
174 Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg
175           50          55          60
176           65          70          75          80
177 cag acc gtg cgc gcc ctc agg atg gag ttc gtg tcc gag gtg cag agg        240
178 Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg
179           65          70          75          80
180           85          90          95
181 aag gtg cac gag gcc cga gcc ggg gtt ctg gcg gag cgc aag gcc ctg        288
182 Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu
183           85          90          95
184           100         105         110
185 aag gac gcc gcc gag cac cgc gag ctg atg gcc tgg aac cag gcg gag        336
186 Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu
187           100         105         110
188           115         120         125
189 aac cgg cgg ctg cac gag ctg cgg ata gcg agg ctg cgg cag gag gag        384
190 Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu
191           115         120         125
192           130         135         140
193 cgg gag cag gag cag cgg ttg gag cag gcc cgc aag gcc gaa        432
194 Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu
195           130         135         140
196           145         150         155         160
197 gag gtg cag gcc tgg gcg cag cgc aag gag cgg gaa gtg ctg cag ctg        480
198 Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu
199           145         150         155         160
200           165         170         175
201 cag gaa gag gtg aaa aac ttc atc acc cga gag aac ctg gag gca cgg        528
202 Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
203           165         170         175
204           180         185         190
205 gtg gaa gca gca ttg gac tcc cgg aag aac tac aac tgg gcc atc acc        576
206 Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr
207           180         185         190
208           195         200         205
209 aga gag ggg ctg gtg gtc agg cca caa cgc agg gac tcc tag ggg ccc        624
210 Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser Gly Pro
211           195         200         205
212           210         215         220
213 agt aag gac agt gcc cgc cag gga cca tgt atg tat cat ggc gga aga        672
214 Ser Lys Asp Ser Ala Arg Gln Gly Pro Cys Met Tyr His Gly Gly Arg
215           210         215         220
216           225         230         235
217 gtt ggc cct gac ctg gaa taa agc agt tgg tgt tgc tta tga gga agg
218 Val Gly Pro Asp Leu Glu Ser Ser Trp Cys Cys Leu Gly Arg
219           225         230         235

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221	ttc	agc	ctt	atc	cag	cac	agc	ctt	cac	gtt	ttg	ccc	tct	gct	gtc	acc	768	
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223	240				245					250							816	
225	act	tgg	tca	gaa	act	tcc	aaa	cgc	agt	gcc	ctg	ttc	tgc	cgg	tgt	gta		
226	Thr	Trp	Ser	Glu	Thr	Ser	Lys	Arg	Ser	Ala	Leu	Phe	Cys	Arg	Cys	Val		
227	255				260					265							864	
229	aag	cct	cag	cgc	acc	agg	aga	ccc	tag	agt	gtt	ttc	cat	ctc	aca	gag		
230	Lys	Pro	Gln	Arg	Thr	Arg	Arg	Pro		Ser	Gly	Phe	His	Leu	Thr	Glu		
231	270				275					280							912	
233	aat	cag	aca	ggc	cac	agc	ccc	ctc	agg	cag	cca	ggt	cat	ctg	agt	atc		
234	Asn	Gln	Thr	Gly	His	Ser	Pro	Leu	Arg	Gln	Pro	Gly	His	Leu	Ser	Ile		
235	285				290					295				300				
237	att	aag	agt	agt	gat	ggg	aag	att	aca	gtc	tga	ggg	cca	aac	gtg	cct	960	
238	Ile	Lys	Ser	Ser	Asp	Gly	Lys	Ile	Thr	Val		Gly	Pro	Asn	Val	Pro		
239	305				310					315								
241	gct	tcc	tgt	ttt	tgt	aaa	taa	agt	ttt	gtt	gga	aca	/ca				998	
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247	<211>	LENGTH:	205															
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262					35				40			45						
265	Asp	Pro	Ala	Glu	Phe	Phe	Val	Leu	Met	Glu	Arg	Tyr	Gln	His	Tyr	Arg		
266					50				55			60						
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273	Lys	Val	His	Glu	Ala	Arg	Ala	Gly	Val	Leu	Ala	Glu	Arg	Lys	Ala	Leu		
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277	Lys	Asp	Ala	Ala	Glu	His	Arg	Glu	Leu	Met	Ala	Trp	Asn	Gln	Ala	Glu		
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282					115				120			125						
285	Arg	Glu	Gln	Glu	Gln	Arg	Gln	Ala	Leu	Glu	Gln	Ala	Arg	Lys	Ala	Glu		
286					130				135			140						
289	Glu	Val	Gln	Ala	Trp	Ala	Gln	Arg	Lys	Glu	Arg	Glu	Val	Leu	Gln	Leu		
290	145					150				155			160					
293	Gln	Glu	Glu	Val	Lys	Asn	Phe	Ile	Thr	Arg	Glu	Asn	Leu	Glu	Ala	Arg		
294					165				170			175						
297	Val	Glu	Ala	Ala	Leu	Asp	Ser	Arg	Lys	Asn	Tyr	Asn	Trp	Ala	Ile	Thr		
298					180				185			190						
301	Arg	Glu	Gly	Leu	Val	Val	Arg	Pro	Gln	Arg	Arg	Asp	Ser					
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305 <210> SEQ ID NO: 5
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307 <212> TYPE: PRT
308 <213> ORGANISM: Rattus sp.
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317 20
320 <210> SEQ ID NO: 6
321 <211> LENGTH: 6
322 <212> TYPE: PRT
323 <213> ORGANISM: Rattus sp.
325 <400> SEQUENCE: 6
327 Ser Ser Trp Cys Cys Leu
328 1 5
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 42
333 <212> TYPE: PRT
334 <213> ORGANISM: Rattus sp.
336 <400> SEQUENCE: 7
338 Gly Arg Phe Ser Leu Ile Gln His Ser Leu His Val Leu Pro Ser Ala
339 1 5 10 15
342 Val Thr Thr Trp Ser Glu Thr Ser Lys Arg Ser Ala Leu Phe Cys Arg
343 20 25 30
346 Cys Val Lys Pro Gln Arg Thr Arg Arg Pro
347 35 40
350 <210> SEQ ID NO: 8
351 <211> LENGTH: 33
352 <212> TYPE: PRT
353 <213> ORGANISM: Rattus sp.
355 <400> SEQUENCE: 8
357 Ser Gly Phe His Leu Thr Glu Asn Gln Thr Gly His Ser Pro Leu Arg
358 1 5 10 15
361 Gln Pro Gly His Leu Ser Ile Ile Lys Ser Ser Asp Gly Lys Ile Thr
362 20 25 30
365 Val
369 <210> SEQ ID NO: 9
370 <211> LENGTH: 11
371 <212> TYPE: PRT
372 <213> ORGANISM: Rattus sp.
374 <400> SEQUENCE: 9
376 Gly Pro Asn Val Pro Ala Ser Cys Phe Cys Lys
377 1 5 10
380 <210> SEQ ID NO: 10
381 <211> LENGTH: 5
382 <212> TYPE: PRT
383 <213> ORGANISM: Rattus sp.
385 <400> SEQUENCE: 10

VERIFICATION SUMMARY

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